What is claimed is:

1. A computer implemented method for determining the genotype of a sample comprising:
Obtaining a plurality of sample probe intensities reflecting the hybridization between the sample and a plurality of probes;
Determining a tentative genotype based upon the sample probe intensities; and
Accepting the tentative genotype as the genotype of the sample if the pattern of the sample probe intensities is similar to that of reference probe intensities for the tentative genotype.

2. The method of Claim 1 wherein the accepting comprising calculating linear correlation coefficient between the sample probe intensities and reference probe intensities; and accepting the tentative genotype as the genotype of the sample if the linear correlation coefficient is greater than a threshold value.

3. The method of Claim 2 wherein the threshold value is at least 0.8.

4. The method of Claim 3 wherein the threshold value is at least 0.9.

5. The method of Claim 4 wherein the threshold value is at least 0.95.

6. The method of Claim 2 wherein the tentative genotype is determined based upon relative allele signal.

7. The method of Claim 6 wherein the probes are immobilized on a substrate at a density of at least 400 probes per cm^2.

8. The method of Claim 7 wherein the probes are immobilized on a substrate at a density of at least 1000 probes per cm^2.

9. The method of Claim 8 wherein the reference genotype is a homozygous genotype.

10. The method of Claim 8 wherein the reference genotype is a heterozygous genotype.

11. The method of Claim 8 wherein the probes contain probes designed to be perfect match for a first genotype and a second genotype.

12. The method of Claim 11 wherein the probes contain probes designed to be mismatch for a first genotype and a second genotype.

13. A computer implemented method for determining the genotype of a sample comprising:

Obtaining a plurality of sample probe intensities reflecting the hybridization between the sample and a plurality of probes; and

Determining whether the pattern of the sample probe intensities is similar to that of reference probe intensities, wherein the reference probe intensities reflect the hybridization between the plurality of probes and a reference sample having a reference genotype.

14. The method of Claim 13 wherein the determining comprising calculating correlation coefficient between the sample probe intensities and reference probe intensities; and indicating that the genotype of the sample is the same as the reference genotype, if the correlation coefficient is greater than a threshold value.

15. The method of Claim 14 wherein the threshold value is at least 0.8.

16. The method of Claim 15 wherein the threshold value is at least 0.9

17. The method of Claim 16 wherein the threshold value is at least 0.95.

18. A system for determining the genotype of a sample comprising:
a processor; and
a memory coupled with the least one processor, the memory storing a plurality of machine instructions that cause the processor to perform logical steps, wherein the logical steps include:
Obtaining a plurality of sample probe intensities reflecting the hybridization between the sample and a plurality of probes;
Determining a tentative genotype based upon the sample probe intensities; and
Accepting the tentative genotype as the genotype of the sample if the pattern of the sample probe intensities is similar to that of reference probe intensities for the tentative genotype.

19. The system of Claim 18 wherein the accepting comprising calculating linear correlation coefficient between the sample probe intensities and reference probe intensities; and accepting the tentative genotype as the genotype of the sample if the linear correlation coefficient is greater than a threshold value.

20. The system of Claim 19 wherein the threshold value is at least 0.8.

21. The system of Claim 20 wherein the threshold value is at least 0.9.

22. The system of Claim 21 wherein the threshold value is at least 0.95.

23. The system of Claim 22 wherein the tentative genotype is determined based upon relative allele signal.

24. The system of Claim 23 wherein the probes are immobilized on a substrate at a density of at least 400 probes per cm^2.

25. The system of Claim 24 wherein the probes are immobilized on a substrate at a density of at least 1000 probes per cm^2.

26. The system of Claim 25 wherein the reference genotype is a homozygous genotype.

27. The system of Claim 26 wherein the reference genotype is a heterozygous genotype.

28. The system of Claim 27 wherein the probes contain probes designed to be perfect match for a first genotype and a second genotype.

29. The method of Claim 28 wherein the probes contain probes designed to be mismatch for a first genotype and a second genotype.

30. A system for determining the genotype of sample comprising:
a processor; and
a memory coupled with the least one processor, the memory storing a plurality of machine instructions that cause the processor to perform logical steps, wherein the logical steps include:
Obtaining a plurality of sample probe intensities reflecting the hybridization between the sample and a plurality of probes; and
Determining whether the pattern of the sample probe intensities is similar to that of reference probe intensities, wherein the reference probe intensities reflect the

hybridization between the plurality of probes and a reference sample having a reference genotype.

31. The system of Claim 31 wherein the determining comprising calculating correlation coefficient between the sample probe intensities and reference probe intensities; and indicating that the genotype of the sample is the same as the reference genotype, if the correlation coefficient is greater than a threshold value.

32. The system of Claim 31 wherein the threshold value is at least 0.8.

33. The system of Claim 32 wherein the threshold value is at least 0.9.

34. The system of Claim 33 wherein the threshold value is at least 0.95.

35. A computer readable medium comprising computer-executable instructions for performing the method for determining the genotype of a sample comprising:
Obtaining a plurality of sample probe intensities reflecting the hybridization between the sample and a plurality of probes;
Determining a tentative genotype based upon the sample probe intensities; and
Accepting the tentative genotype as the genotype of the sample if the pattern of the sample probe intensities is similar to that of reference probe intensities for the tentative genotype.

36. The computer readable medium of Claim 35 wherein the accepting comprising calculating linear correlation coefficient between the sample probe intensities and reference probe intensities; and accepting the tentative genotype as the genotype of the sample if the linear correlation coefficient is greater than a threshold value.

37. The computer readable medium of Claim 36 wherein the threshold value is at least 0.8.

38. The computer readable medium of Claim 37 wherein the threshold value is at least 0.9.

39. The computer readable medium of Claim 38 wherein the threshold value is at least 0.95.

40. The computer readable medium of Claim 39 wherein the tentative genotype is determined based upon relative allele signal.

41. The computer readable medium of Claim 40 wherein the probes are immobilized on a substrate at a density of at least 400 probes per cm^2.

42. The computer readable medium of Claim 42 wherein the probes are immobilized on a substrate at a density of at least 1000 probes per cm^2.

43. The computer readable medium of Claim 42 wherein the reference genotype is a homozygous genotype.

44. The computer readable medium of Claim 43 wherein the reference genotype is a heterozygous genotype.

45. The computer readable medium of Claim 42 wherein the probes contain probes designed to be perfect match for a first genotype and a second genotype.

46. The computer readable medium of Claim 45 wherein the probes contain probes designed to be mismatch for a first genotype and a second genotype.

47. A computer readable medium comprising computer-executable instructions for performing the methods comprising:
Obtaining a plurality of sample probe intensities reflecting the hybridization between the sample and a plurality of probes; and
Determining whether the pattern of the sample probe intensities is similar to that of reference probe intensities, wherein the reference probe intensities reflect the hybridization between the plurality of probes and a reference sample having a reference genotype.

48. The computer readable medium of Claim 47 wherein the determining comprising calculating correlation coefficient between the sample probe intensities and reference probe intensities; and indicating that the genotype of the sample is the same as the reference genotype, if the correlation coefficient is greater than a threshold value.

49. The computer readable medium of Claim 48 wherein the threshold value is at least 0.8.

50. The computer readable medium of Claim 49 wherein the threshold value is at least 0.9

51. The computer readable medium of Claim 50 wherein the threshold value is at least 0.95.